

SEQUENCE LISTING

<110> Rory A.J. Curtis

<120> 55053, A Novel Human Eukaryotic Kinase
and Uses Therefor

<130> MNI-206

<150> 60/248,893

<151> 2000-11-15

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<212> DNA

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<221> CDS

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Gly Gly Ser Pro Ala Tyr His Leu Pro His Pro His Pro His Pro Pro
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cag cac gcc caa tat gtg ggc ccc tat cgg ctg gag aag acg ctg ggc 208
Gln His Ala Gln Tyr Val Gly Pro Tyr Arg Leu Glu Lys Thr Leu Gly
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aaa gga cag aca ggg ctg gtt aaa ctc ggg gtc cac tgc atc acg ggt 256
Lys Gly Gln Thr Gly Leu Val Lys Leu Gly Val His Cys Ile Thr Gly
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cag aag gtc gcc atc aag atc gtg aac cgg gag aag ctg tcg gag tcg 304
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Val Leu Met Lys Val Glu Arg Glu Ile Ala Ile Leu Lys Leu Ile Glu
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His Pro His Val Leu Lys Leu His Asp Val Tyr Glu Asn Lys Lys Tyr
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ctg gta aag aag ggg aga ctg acg ccc aag gag gcc cga aag ttc ttc	496
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cgc cag att gtg tct gcg ctg gac ttc tgc cac agc tac tcc atc tgc	544
Arg Gln Ile Val Ser Ala Leu Asp Phe Cys His Ser Tyr Ser Ile Cys	
140 145 150	
cac aga gac cta aag ccc gag aac ctg ctt ttg gat gag aaa aac aac	592
His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Asp Glu Lys Asn Asn	
155 160 165	
atc cgc att gca gac ttc ggc atg gcg tcc ctg cag gtg ggg gac agc	640
Ile Arg Ile Ala Asp Phe Gly Met Ala Ser Leu Gln Val Gly Asp Ser	
170 175 180 185	
ctc ctg gag acc agc tgc ggg tcc ccc cat tat gcg tgt cca gag gtg	688
Leu Leu Glu Thr Ser Cys Gly Ser Pro His Tyr Ala Cys Pro Glu Val	
190 195 200	
att aag ggg gaa aaa tat gat ggc cgc cgg gca gac atg tgg agc tgt	736
Ile Lys Gly Glu Lys Tyr Asp Gly Arg Arg Ala Asp Met Trp Ser Cys	
205 210 215	
gga gtc atc ctc ttc gcc ctg ctc gtg ggg gct ctg ccc ttt gat gac	784
Gly Val Ile Leu Phe Ala Leu Leu Val Gly Ala Leu Pro Phe Asp Asp	
220 225 230	
gac aac ctc cgc cag ctg ctg gag aag gtg aaa cgg ggc gtc ttc cac	832
Asp Asn Leu Arg Gln Leu Leu Glu Lys Val Lys Arg Gly Val Phe His	
235 240 245	
atg ccc cac ttc att cct cca gat tgc cag agc ctc ctg agg gga atg	880
Met Pro His Phe Ile Pro Pro Asp Cys Gln Ser Leu Leu Arg Gly Met	
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atc gaa gtg gag ccc gaa aaa agg ctc agt ctg gag caa att cag aaa	928
Ile Glu Val Glu Pro Glu Lys Arg Leu Ser Leu Glu Gln Ile Gln Lys	
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cat cct tgg tac cta ggc ggg aaa cac gag cca gac ccg tgc ctg gag	976
His Pro Trp Tyr Leu Gly Gly Lys His Glu Pro Asp Pro Cys Leu Glu	
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Pro Ala Pro Gly Arg Arg Val Ala Met Arg Ser Leu Pro Ser Asn Gly	
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Glu Leu Asp Pro Asp Val Leu Glu Ser Met Ala Ser Leu Gly Cys Phe	
315 320 325	
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Arg Asp Arg Glu Arg Leu His Arg Glu Leu Arg Ser Glu Glu Glu Asn	
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Pro Ser Cys Glu Asp Gln Asp Leu Pro Pro Arg Asn Asp Val Asp Pro	
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Pro Arg Lys Arg Val Asp Ser Pro Met Leu Ser Arg His Gly Lys Arg	
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Gly Gly Gly Ser Pro Val Pro Thr Arg Arg Ala Leu Glu Met Ala Gln	
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His Ser Gln Arg Ser Arg Ser Val Ser Gly Ala Ser Thr Gly Leu Ser	
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Lys Thr Gln Thr Leu Pro Ser Arg Gly Pro Arg Gly Gly Gly Ala Gly	
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Pro Ser Pro Gly Gly Gly Val Gly Gly Ala Ala Trp Arg Ser Arg Leu	
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Lys Met Gln Val Pro Thr Ala Glu Glu Met Ser Ser Leu Thr Pro Glu	
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Ser Ser Pro Glu Leu Ala Lys Arg Ser Trp Phe Gly Asn Phe Ile Ser	
590 595 600	

- 4 -

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agc agc atc aaa gca gac atc gtc cat gcc ttt ctg tgc atc ccc agc	1984
Ser Ser Ile Lys Ala Asp Ile Val His Ala Phe Leu Ser Ile Pro Ser	
620 625 630	
ctg agt cac agt gtg ctg tca cag acc agc ttc agg gcc gag tac aag	2032
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Pro Ser Arg Arg Phe Lys Arg Val Val Glu Thr Ile Gln Ala Gln Leu	
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Leu Ser Thr His Asp Gln Pro Ser Val Gln Ala Leu Ala Asp Glu Lys	
715 720 725	
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Asn Gly Ala Gln Thr Arg Pro Ala Gly Ala Pro Pro Arg Ser Leu Gln	
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Gly Pro Pro Lys Asp Lys Lys Leu Leu Ala Thr Asn Gly Thr Pro Leu	
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Val	Asn	Arg	Glu	Lys	Leu	Ser	Glu	Ser	Val	Leu	Met	Lys	Val	Glu	Arg
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Thr	Pro	Lys	Glu	Ala	Arg	Lys	Phe	Phe	Arg	Gln	Ile	Val	Ser	Ala	Leu
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Asp	Phe	Cys	His	Ser	Tyr	Ser	Ile	Cys	His	Arg	Asp	Leu	Lys	Pro	Glu
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Met	Ala	Ser	Leu	Gln	Val	Gly	Asp	Ser	Leu	Leu	Glu	Thr	Ser	Cys	Gly
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Ser	Pro	His	Tyr	Ala	Cys	Pro	Glu	Val	Ile	Lys	Gly	Glu	Lys	Tyr	Asp
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Glu	Lys	Val	Lys	Arg	Gly	Val	Phe	His	Met	Pro	His	Phe	Ile	Pro	Pro
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Asp	Cys	Gln	Ser	Leu	Leu	Arg	Gly	Met	Ile	Glu	Val	Glu	Pro	Glu	Lys
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Arg	Leu	Ser	Leu	Glu	Gln	Ile	Gln	Lys	His	Pro	Trp	Tyr	Leu	Gly	Gly
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Lys	His	Glu	Pro	Asp	Pro	Cys	Leu	Glu	Pro	Ala	Pro	Gly	Arg	Arg	Val
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305					310					315				320	
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Arg	Glu	Leu	Arg	Ser	Glu	Glu	Glu	Asn	Gln	Glu	Lys	Met	Ile	Tyr	Tyr
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Leu	Pro	Pro	Arg	Asn	Asp	Val	Asp	Pro	Pro	Arg	Lys	Arg	Val	Asp	Ser
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Pro	Met	Leu	Ser	Arg	His	Gly	Lys	Arg	Arg	Pro	Glu	Arg	Lys	Ser	Met
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- 6 -

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465 470 475 480
Arg Gly Pro Arg Gly Gly Gly Ala Gly Glu Gln Pro Pro Pro Pro Ser
485 490 495
Ala Arg Ser Thr Pro Leu Pro Gly Pro Pro Gly Ser Pro Arg Ser Ser
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Gly Gly Thr Pro Leu His Ser Pro Leu His Thr Pro Arg Ala Ser Pro
515 520 525
Thr Gly Thr Pro Gly Thr Thr Pro Pro Pro Ser Pro Gly Gly Gly Val
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Gly Gly Ala Ala Trp Arg Ser Arg Leu Asn Ser Ile Arg Asn Ser Phe
545 550 555 560
Leu Gly Ser Pro Arg Phe His Arg Arg Lys Met Gln Val Pro Thr Ala
565 570 575
Glu Glu Met Ser Ser Leu Thr Pro Glu Ser Ser Pro Glu Leu Ala Lys
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Arg Ser Trp Phe Gly Asn Phe Ile Ser Leu Asp Lys Glu Glu Gln Ile
595 600 605
Phe Leu Val Leu Lys Asp Lys Pro Leu Ser Ser Ile Lys Ala Asp Ile
610 615 620
Val His Ala Phe Leu Ser Ile Pro Ser Leu Ser His Ser Val Leu Ser
625 630 635 640
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660 665 670
Pro Glu Pro Ser Pro Arg Arg Asp Gly Ser Gly Gly Gly Ile Tyr
675 680 685
Ser Val Thr Phe Thr Leu Ile Ser Gly Pro Ser Arg Arg Phe Lys Arg
690 695 700
Val Val Glu Thr Ile Gln Ala Gln Leu Leu Ser Thr His Asp Gln Pro
705 710 715 720
Ser Val Gln Ala Leu Ala Asp Glu Lys Asn Gly Ala Gln Thr Arg Pro
725 730 735
Ala Gly Ala Pro Pro Arg Ser Leu Gln Pro Pro Pro Gly Arg Pro Asp
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35 40 45	
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50 55 60	
gtg aac cgg gag aag ctg tgc gag tgc gtg ctg atg aag gtg gag cgg Val Asn Arg Glu Lys Leu Ser Glu Ser Val Leu Met Lys Val Glu Arg	240
65 70 75 80	
gag atc gcc atc ctg aag ctc atc gaa cac cca cat gtc ctc aag ctc Glu Ile Ala Ile Leu Lys Leu Ile Glu His Pro His Val Leu Lys Leu	288
85 90 95	
cac gac gtc tac gag aac aag aaa tat ttg tac ctg gtt ctg gag cac His Asp Val Tyr Glu Asn Lys Lys Tyr Leu Tyr Leu Val Leu Glu His	336
100 105 110	
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115 120 125	
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130 135 140	
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Arg Leu Ser Leu Glu Gln Ile Gln Lys His Pro Trp Tyr Leu Gly Gly	
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Lys His Glu Pro Asp Pro Cys Leu Glu Pro Ala Pro Gly Arg Arg Val	
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Glu Val Leu Ser Ile Thr Asp Ala Gly Gly Gly Gly Ser Pro Val Pro	
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485 490 495	

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Thr Gly Thr Pro Gly Thr Thr Pro Pro Pro Ser Pro Gly Gly Gly Val	
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Phe Leu Val Leu Lys Asp Lys Pro Leu Ser Ser Ile Lys Ala Asp Ile	
610 615 620	
gtc cat gcc ttt ctg tcg atc ccc agc ctg agt cac agt gtg ctg tca	1920
Val His Ala Phe Leu Ser Ile Pro Ser Leu Ser His Ser Val Leu Ser	
625 630 635 640	
cag acc agc ttc agg gcc gag tac aag gcc agt ggc ggc ccc tcc gtc	1968
Gln Thr Ser Phe Arg Ala Glu Tyr Lys Ala Ser Gly Gly Pro Ser Val	
645 650 655	
ttc caa aag ccc gtc cgc ttc cag gtg gac atc agc tcc tct gag ggt	2016
Phe Gln Lys Pro Val Arg Phe Gln Val Asp Ile Ser Ser Ser Glu Gly	
660 665 670	
cca gag ccc tcc ccg cga cgg gac ggc agc gga ggt ggt ggc atc tac	2064
Pro Glu Pro Ser Pro Arg Arg Asp Gly Ser Gly Gly Gly Gly Ile Tyr	
675 680 685	
tcc gtc acc ttc act ctc atc tcg ggt ccc agc cgt cgg ttc aag cga	2112
Ser Val Thr Phe Thr Leu Ile Ser Gly Pro Ser Arg Arg Phe Lys Arg	
690 695 700	
gtg gtg gag acc atc cag gca cag ctc ctg agc act cat gac cag ccc	2160
Val Val Glu Thr Ile Gln Ala Gln Leu Leu Ser Thr His Asp Gln Pro	
705 710 715 720	
tcc gtg cag gcc ctg gca gac gag aag aac ggg gcc cag acc cgg cct	2208
Ser Val Gln Ala Leu Ala Asp Glu Lys Asn Gly Ala Gln Thr Arg Pro	
725 730 735	

- 10 -

gct ggt gcc cca ccc cga agc ctg cag ccc cca ccc ggc cgc cca gac 2256
 Ala Gly Ala Pro Pro Arg Ser Leu Gln Pro Pro Pro Gly Arg Pro Asp
 740 745 750

cca gag ctg agc agc tct ccc cgc cga ggc ccc ccc aag gac aag aag 2304
 Pro Glu Leu Ser Ser Ser Pro Arg Arg Gly Pro Pro Lys Asp Lys Lys
 755 760 765

ctc ctg gcc acc aac ggg acc cct ctg ccc 2334
 Leu Leu Ala Thr Asn Gly Thr Pro Leu Pro
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 Lys Ala Lys His Lys Thr Gly Lys Ile Val Ala Val Lys Ile Leu Lys
 20 25 30

- 11 -

Lys Glu Ser Leu Ser Leu Arg Glu Ile Gln Ile Leu Lys Arg Leu Ser
 35 40 45
 His Pro Asn Ile Val Arg Leu Leu Gly Val Phe Glu Asp Thr Asp Asp
 50 55 60
 His Leu Tyr Leu Val Met Glu Tyr Met Glu Gly Gly Asp Leu Phe Asp
 65 70 75 80
 Tyr Leu Arg Arg Asn Gly Pro Leu Ser Glu Lys Glu Ala Lys Lys Ile
 85 90 95
 Ala Leu Gln Ile Leu Arg Gly Leu Glu Tyr Leu His Ser Asn Gly Ile
 100 105 110
 Val His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu Asn Gly
 115 120 125
 Thr Val Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Leu Glu Lys Leu
 130 135 140
 Thr Thr Phe Val Gly Thr Pro Trp Tyr Met Met Ala Pro Glu Val Ile
 145 150 155 160
 Leu Glu Gly Arg Gly Tyr Ser Ser Lys Val Asp Val Trp Ser Leu Gly
 165 170 175
 Val Ile Leu Tyr Glu Leu Leu Thr Gly Gly Pro Leu Phe Pro Gly Ala
 180 185 190
 Asp Leu Pro Ala Phe Thr Gly Gly Asp Glu Val Asp Gln Leu Ile Ile
 195 200 205
 Phe Val Leu Lys Leu Pro Phe Ser Asp Glu Leu Pro Lys Thr Arg Ile
 210 215 220
 Asp Pro Leu Glu Glu Leu Phe Arg Ile Lys Lys Arg Arg Leu Pro Leu
 225 230 235 240
 Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu Lys Lys Cys Leu
 245 250 255
 Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr Ala Lys Glu Ile
 260 265 270
 Leu Asn His Pro Trp Phe
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<220>
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 Glu Asp Glu Glu Lys Ile Glu Gln Leu Val Glu Met Gly Phe Asp Arg
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 20 25 30
 Arg Ala Ala Glu Trp Leu Leu Ser His
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<220>
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Lys Glu Arg Ile Leu Arg Glu Ile Lys Ile Leu Lys Lys Asp His Pro
          35          40          45
Asn Ile Val Lys Leu Tyr Asp Val Phe Glu Asp Asp Lys Leu Tyr Leu
          50          55          60
Val Met Glu Tyr Cys Glu Gly Asp Leu Gly Asp Leu Phe Asp Leu Leu
65          70          75          80
Lys Lys Arg Gly Arg Arg Gly Leu Arg Lys Val Leu Ser Glu Glu Ala
          85          90          95
Arg Phe Tyr Phe Arg Gln Ile Leu Ser Ala Leu Glu Tyr Leu His Ser
          100          105          110
Gln Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp
          115          120          125
Ser His Val Lys Leu Ala Asp Phe Gly Leu Ala Arg Gln Leu Thr Thr
          130          135          140
Phe Val Gly Thr Pro Glu Tyr Met Ala Pro Glu Val Leu Gly Tyr Gly
145          150          155          160
Lys Pro Ala Val Asp Ile Trp Ser Leu Gly Cys Ile Leu Tyr Glu Leu
          165          170          175
Leu Thr Gly Lys Lys Pro Pro Phe Pro Gln Leu Asp Leu Ile Phe Lys Lys
          180          185          190
Ile Gly Ser Pro Glu Ala Lys Asp Leu Ile Lys Lys Leu Leu Val Lys
          195          200          205
Asp Pro Glu Lys Arg Leu Thr Ala Glu Ala Leu Glu Asp Glu Leu Asp
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Ile Lys Ala His Pro Phe Phe
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<223> tyrkin_6 domain

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          20          25          30
Ala Lys Glu Glu Phe Leu Arg Glu Ala Lys Ile Met Lys Lys Leu Gly
          35          40          45
Gly Lys His Pro Asn Ile Val Lys Leu Leu Gly Val Cys Thr Glu Glu
          50          55          60
Gly Arg Arg Phe Met Glu Val Glu Pro Leu Met Ile Val Met Glu Tyr
65          70          75          80
Met Glu Gly Gly Asp Leu Leu Asp Tyr Leu Arg Lys Asn Arg Pro Lys
          85          90          95
Leu Ser Leu Ser Asp Leu Leu Ser Phe Ala Leu Gln Ile Ala Lys Gly
          100          105          110
Met Glu Tyr Leu Glu Ser Lys Asn Phe Val His Arg Asp Leu Ala Ala
          115          120          125
Arg Asn Cys Leu Val Gly Glu Asn Lys Val Val Lys Ile Ser Asp Phe
          130          135          140

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